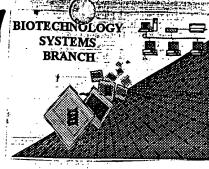BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

RECEIVED

JAN 1 0 2001

TECH CENTER

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/265,540 C_

Source: _1643_

Date Processed by STIC: _1/2/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error-Summary

ERROR DETECTED   **SUGGESTED CORRECTION**

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

```
        RAW SEQUENCE LISTING                 DATE: 01/03/2001
        PATENT APPLICATION:  US/09/265,540C  TIME: 12:53:41

        Input Set : A:\804k.app
        Output Set: N:\CRF3\01022001\I265540C.raw

 3  <110> APPLICANT: Parham, Christi L.
 4         Moore, Kevin W.
 5         Hurgolo, Nicholas J.
 6         Bazan, J. Fernando
 8  <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
10  <130> FILE REFERENCE: DX0804K
12  <140> CURRENT APPLICATION NUMBER: 09/265,540C
13  <141> CURRENT FILING DATE: 1999-03-08
15  <160> NUMBER OF SEQ ID NOS: 6
17  <170> SOFTWARE: PatentIn Ver. 2.0
19  <210> SEQ ID NO: 1
20  <211> LENGTH: 1381
21  <212> TYPE: DNA
22  <213> ORGANISM: primate
24  <220> FEATURE:
25  <221> NAME/KEY: CDS
26  <222> LOCATION: (132)..(1064)
28  <220> FEATURE:
29  <221> NAME/KEY: misc_feature
30  <222> LOCATION: (567)
31  <223> OTHER INFORMATION: n at position 567; n may be A, C, G, or T;
32         translated amino acid depends on genetic code
34  <220> FEATURE:
35  <221> NAME/KEY: misc_feature
36  <222> LOCATION: (573)
37  <223> OTHER INFORMATION: n at position 573; n may be A, C, G, or T;
38         translated amino acid depends on genetic code
40  <220> FEATURE:
41  <221> NAME/KEY: misc_feature
42  <222> LOCATION: (1336)
43  <223> OTHER INFORMATION: n at position 1336; n may be A,C, G, or T;
44         translated amino acid depends on genetic code
46  <220> FEATURE:
47  <221> NAME/KEY: misc_feature
48  <222> LOCATION: (1342)
49  <223> OTHER INFORMATION: n at position 1342; n may be A, C, G, or T;
50         translated amino acid depends on genetic code
52  <220> FEATURE:
53  <221> NAME/KEY: misc_feature
54  <222> LOCATION: (1369)
55  <223> OTHER INFORMATION: n at position 1369; n may be A, C, G, or T;
56         translated amino acid depends on genetic code
58  <400> SEQUENCE: 1
59  tcgaccacg cgtccgcgct tcgactcaga cctcagctcc aacatatgca ttctgaagaa  60
61  agatgnctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120
63  gagtctacca a atg gag act ttc aca atg gtt cta gaa gaa atc tgg aca  170
64                 Met Glu Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr
```

RAW SEQUENCE LISTING   DATE: 01/02/2001
PATENT APPLICATION: US/09/265,540C   TIME: 12:53:41

Input Set : A:\804k.app
Output Set: N:\CRF3\01022001\1265540C.raw

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65              1              5              10
67 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca    218
68 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr
69     15              20              25
71 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca    266
72 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
73  30              35              40              45
75 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga    314
76 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
77          50              55              60
79 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg    362
80 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
81          65              70              75
83 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa    410
84 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
85          80              85              90
87 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac    458
88 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
89      95              100             105
91 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc    506
92 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
93 110             115             120             125
95 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct    554
96 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
97          130             135             140
99 ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag    602
100 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
101         145             150             155
103 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag   650
104 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
105         160             165             170
107 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca   698
108 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
109         175             180             185
111 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc   746
112 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
113 190             195             200             205
115 cag aca ttc gtg aag gcc att ggg agg tac agc gcc ttc agc cag aca   794
116 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
117         210             215             220
119 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg   842
120 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
121         225             230             235
123 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc   890
124 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
125         240             245             250
127 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg   938
128 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
129         255             260             265
```

Please align amino acids directly under corresponding codon.

RAW SEQUENCE LISTING   DATE: 01/02/2001
PATENT APPLICATION: US/09/265,540C   TIME: 12:53:41

Input Set : A:\804k.app
Output Set: N:\CRF3\01022001\1265540C.raw

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131 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc     986
132 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
133 270                   275                   280                   285
135 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct     1034
136 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
137                       290                   295                   300
139 cct gag gaa ctc ctc aga gcc tgg atc tca taggtttgcg gaagggccca       1084
140 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
141                       305                   310
143 ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gagaggacaa gttgtgtttc  1144
145 tgtttttccgc cacgggacaag ggatgagaga agtaggaaga gcctgttgtc tacaagtcta 1204
147 gaagcaaacca tcagaggcag ggtggttcgt ckaacaagac aaytgactga ggytakrggu 1264
149 gwtgtgacct ctagactktg ggstkscayt tgcwtgrytg agcaacccta ggaaaagtga 1324
151 cttcatccct tnggtccnaa gtttctcat ctgtaatggg ggatncctac aaaactg      1381
```

154 <210> SEQ ID NO: 2
155 <211> LENGTH: 311
156 <212> TYPE: PRT
157 <213> ORGANISM: primate
159 <400> SEQUENCE: 2

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160 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
161  1                   5                   10                   15
163 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
164                  20                   25                   30
166 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
167                  35                   40                   45
169 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
170         50                   55                   60
172 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
173  65                   70                   75                   80
175 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
176                  85                   90                   95
178 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
179                 100                  105                  110
181 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
182         115                  120                  125
184 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
185         130                  135                  140
187 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly   W-->
188 145                  150                  155                  160
190 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala   W-->
191                 165                  170                  175
193 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
194                 180                  185                  190
196 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
197                 195                  200                  205
199 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val   W-->
200         210                  215                  220
202 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe   W-->
203                 225                  230                  235                  240
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[handwritten: see item 10 on Error Summary Sheet]

RAW SEQUENCE LISTING   DATE: 01/02/2001
PATENT APPLICATION: US/09/265,540C   TIME: 12:53:41

Input Set : A:\804k.app
Output Set: N:\CRF3\01022001\I265540C.raw

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205 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
206            245             250              255
208 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
209           260               265             270
211 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
212           275              280              285
214 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Gln Glu
215        290              295              300
217 Leu Leu Arg Ala Trp Ile Ser
218 305              310
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 1244
223 <212> TYPE: DNA
224 <213> ORGANISM: primate
226 <220> FEATURE:
227 <221> NAME/KEY: CDS
228 <222> LOCATION: (2)..(694)
230 <400> SEQUENCE: 3
231 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49
232   Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
233   1              5              10               15
235 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc    97
236 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
237           20               25              30
239 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc   145
240 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
241           35               40              45
243 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay   193
244 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
245           50               55              60
247 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac   241
248 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
249   65               70              75               80
251 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa   289
252 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
253           85               90              95
255 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc   337
256 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
257           100              105             110
259 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg   385
260 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
261           115              120             125
263 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg   433
264 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
265      130              135             140
267 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc   481
268 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
269 145              150              155             160
271 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc   529
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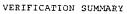
RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001
TIME: 12:53:41

Input Set : A:\804k.app
Output Set: N:\CRF3\01022001\I265540C.raw

```
272 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
273              165                  170                  175
275 gaa gag tat ctg aag gtc tcg agc cag cct atc cta gag gcc ctg gac      577
276 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
277              180                  185                  190
279 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt      625
280 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
281              195                  200                  205
283 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc      673
284 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
285      210                  215                  220
287 caa aac tct ggt gca gtc tgc tagcctgtgg ggtaaggget ctgagccgag        724
288 Gln Asn Ser Gly Ala Val Cys
289 225                  230
291 gaagctgctg atgtccatgt cagcacttta tggaatccgg tcctccattt tcctgtcccc  784
293 aaaaggcccg tcagtgcctg tgaagatgta acgggtctca tggggcgac aagcttattg   844
295 attttttttct tcaaactaag agtttttctaa tcatacgcgt ttttagaata attctacaga  904
297 tatgtccccg aaagattaag attttctctta aacactaaaa agacatgtaa ttatttgtta   964
299 gcaaatgggc gtctggcacg cctctgacac ttttttcgtca gcagccagga cacgaggtcc  1024
301 cctcctgat gaagccctc gggcagacca tgtcacatgt cccagcctac cccaagqaqq     1081
303 gacattaagt ggccttctt catatccaaa cacctggctt gaaatgtgat tagcctctta    1144
305 aatagtttca cagagattaa gcctttttt ccccaagtg aggaataaaa gactataatt    1204
307 aactttttaa aaaaaaaaa aaaaaaaaa aaaaaaaaa                            1244
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 231
312 <212> TYPE: PRT
313 <213> ORGANISM: primate
315 <400> SEQUENCE: 4
316 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
317   1                  5                  10                  15
319 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
320              20                  25                  30
322 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
323              35                  40                  45
```

W-->
```
325 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
326      50                  55                  60
328 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
329 65                  70                  75                  80
331 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
332              85                  90                  95
334 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
335              100                  105                  110
337 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
338              115                  120                  125
340 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
341      130                  135                  140
343 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
344 145                  150                  155                  160
346 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
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(handwritten: "Item 10")

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001
TIME: 12:53:42

Input Set : A:\804k.app
Output Set: N:\CRF3\01022001\I265540C.raw

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L:99  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:187 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:187 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:199 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:244 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:244 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:325 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:325 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:325 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:325 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:325 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
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